

Figures

Figure 1 - Nucleotide and protein sequence of Aspergillus ochraceus 11 alpha hydroxylase

5	tggaaagtttt tacacttatt atgcccggagc cgaaagattc tgagtcgagg ggttgggaa caacactata agacctacaa ccactggat ttggtaatt tacacggca ttatcaa agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg Met Pro Phe Phe Thr Gly Leu Leu Ala	60 120 172
10	1 att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr 10 15 20 25	220
15	15 att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc Ile Val Val Leu Ala Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser 30 35 40	268
20	20 gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg 45 50 55	316
25	25 cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg Arg Arg Val His Glu Phe Val Glu Asn Ser Lys Ser Leu Leu Ala Arg 60 65 70	364
30	30 ggg agg gaa ttg cac ggg cac gag ccg tac aga ctc atg tct gaa tgg Gly Arg Glu Leu His Gly His Glu Pro Tyr Arg Leu Met Ser Glu Trp 75 80 85	412
35	35 gga tcc ttg att gtc ctg ccc cca gag tgc gcc gac gag ctg cgc aac Gly Ser Leu Ile Val Leu Pro Pro Glu Cys Ala Asp Glu Leu Arg Asn 90 95 100 105	460
40	40 gac cca aga atg gac ttt gag acg ccc acc acc gac gac tcc cac gga Asp Pro Arg Met Asp Phe Glu Thr Pro Thr Asp Asp Ser His Gly 110 115 120	508
45	45 tat atc cct ggc ttc gac gct ctc aac gca gac ccg aac ctg act aaa Tyr Ile Pro Gly Phe Asp Ala Leu Asn Ala Asp Pro Asn Leu Thr Lys 125 130 135	556
50	50 gtg gtc acc aag tac ctc aca aaa gca ttg aac aag ctt act gct ccg Val Val Thr Lys Tyr Leu Thr Lys Ala Leu Asn Lys Leu Thr Ala Pro 140 145 150	604
55	55 atc tcg cat gaa gcg tcc atc gcc atg aaa gcg gtg ctg ggt gac gat Ile Ser His Glu Ala Ser Ile Ala Met Lys Ala Val Leu Gly Asp Asp 155 160 165	652
60	60 cca gat tgg cgt gag atc tac cca gcc aga gac ttg ctc cag ctc gtc Pro Asp Trp Arg Glu Ile Tyr Pro Ala Arg Asp Leu Leu Gln Leu Val 170 175 180 185	700
65	65 gcc cgg atg tcg aca aga gtg ttc ctt ggc gag gaa atg tgc aat aac Ala Arg Met Ser Thr Arg Val Phe Leu Gly Glu Met Cys Asn Asn 190 195 200	748
70	70 cag gat tgg atc caa acc tca tca caa tac gcg gcc ctt gcc ttc ggt Gln Asp Trp Ile Gln Thr Ser Ser Gln Tyr Ala Ala Leu Ala Phe Gly 205 210 215	796
75	75 gtc ggt gac aag ctt aga ata tac ccg aga atg atc aga ccg ata gta Val Gly Asp Lys Leu Arg Ile Tyr Pro Arg Met Ile Arg Pro Ile Val 220 225 230	844
80	80 cat tgg ttc atg cca tcc tgt tgg gag ctg cgc cga tcg ctg cga cgc His Trp Phe Met Pro Ser Cys Trp Glu Leu Arg Arg Ser Leu Arg Arg 235 240 245	892
85	85 tgc cga cag att ctc acg ccg tac att cac aaa cgc aag tcc ctg aag Cys Arg Gln Ile Leu Thr Pro Tyr Ile His Lys Arg Lys Ser Leu Lys 250 255 260 265	940
90	90 ggg acc acg gac gag cag ggc aag ccc ctt atg ttt gat gat tcc atc Gly Thr Thr Asp Glu Gln Gly Lys Pro Leu Met Phe Asp Asp Ser Ile 270 275 280	988

	gag tgg ttc gag cga gag ctg ggt ccc aac cac gac gcg gtc ctg aag Glu Trp Phe Glu Arg Glu Leu Gly Pro Asn His Asp Ala Val Leu Lys 285 290 295	1036
5	cag gtc acg ctc tcc ata gtt gct atc cac acc acg agt gac cta ctc Gln Val Thr Leu Ser Ile Val Ala Ile His Thr Ser Asp Leu Leu 300 305 310	1084
10	ttg cag gcc atg agc gat ctc gcg cag aac ccg aaa gtg cta caa gca Leu Gln Ala Met Ser Asp Leu Ala Gln Asn Pro Lys Val Leu Gln Ala 315 320 325	1132
15	gtg cgc gag gag gtg gtc cga gtg ctg agc acc gag ggg ctc agc aag Val Arg Glu Glu Val Val Arg Val Leu Ser Thr Glu Gly Leu Ser Lys 330 335 340 345	1180
20	gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc Val Ser Leu His Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser 350 355 360	1228
25	cag cgt ctc agg cct acg ctt ctc ggc tcc ttt cgt cgg cag gca acg Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Arg Gln Ala Thr 365 370 375	1276
30	aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga Asn Asp Ile Lys Leu Lys Ser Gly Phe Val Ile Lys Lys Gly Thr Arg 380 385 390	1324
35	gtc gtg atc gac agc acc cat atg tgg aat ccc gag tat tac act gac Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp 395 400 405	1372
40	cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc Pro Leu Gln Tyr Asp Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro 410 415 420 425	1420
45	ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met 430 435 440	1468
50	gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser 445 450 455	1516
55	aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp 460 465 470	1564
60	cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act Arg Leu Pro Asp Gly Phe Lys Pro Gln Pro Leu Asn Ile Gly Met Thr 475 480 485	1612
	tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala 490 495 500 505	1660
	gag atc gat atg gcg agt tta act gtg tag gtcgaacacg aagtccctgat Glu Ile Asp Met Ala Ser Leu Thr Val *	1710
	gaagtgttat tggcagtgg gtgaagcaag tcgcagaaat gtgtaacaat ttataagaat aaaaaa	1770 1776

**Figure 2 - Nucleotide and protein sequence of human
oxidoreductase**

5	atg gga gac tcc cac gtg gac acc agc tcc acc gtg tcc gag gcg gtg Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val 1 5 10 15	48
10	gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser 20 25 30	96
15	ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag aaa aaa Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys 35 40 45	144
20	gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val 50 55 60	192
25	aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile 65 70 75 80	240
30	atc gtg ttc tac ggc tcc cag acg ggg act gca gag gag ttt gcc aac Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn 85 90 95	288
35	cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga ggc atg tca gcg Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala 100 105 110	336
40	gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile 115 120 125	384
45	gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp 130 135 140	432
50	ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp 145 150 155 160	480
55	gtg gat ctc tct ggg gtc aag ttc gcg gtg ttt ggt ctt ggg aac aag Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys 165 170 175	528
60	acc tac gag cac ttc aat gcc atg ggc aag tac gtg gac aag cgg ctg Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu 180 185 190	576
65	gag cag ctc ggc gcc cag cgc atc ttt gag ctg ggg ttg ggc gac gac Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp 195 200 205	624
70	gat ggg aac ttg gag gag gac ttc atc acc tgg cga gag cag ttc tgg Asp Gly Asn Leu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp 210 215 220	672
75	ccg gcc gtg tgt gaa cac ttt ggg gtg gaa gcc act ggc gag gag tcc Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Ser 225 230 235 240	720
80	agc att cgc cag tac gag ctt gtg gtc cac acc gac ata gat gcg gcc Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala 245 250 255	768
85	aag gtg tac atg ggg gag atg ggc cgg ctg aag agc tac gag aac cag Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln 260 265 270	816
90	aag ccc ccc ttt gat gcc aag aat ccg ttc ctg gct gca gtc acc acc Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr 275 280 285	864
95	aac cgg aag ctg aac cag gga acc gag cgc cac ctc atg cac ctg gaa Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu 290 295 300	912
100	ttg gac atc tcg gac tcc aaa atc agg tat gaa tct ggg gac cac gtg Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val	960

	305	310	315	320	
5	gct gtg tac cca gcc aac gac tct gct ctc gtc aac cag ctg ggc aaa Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys 325 330 335				1008
10	atc ctg ggt gcc gac ctg gac gtc gtc atg tcc ctg aac aac ctg gat Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Asn Leu Asp 340 345 350				1056
15	gag gag tcc aac aag aag cac cca ttc ccg tgc cct acg tcc tac cgc Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg 355 360 365				1104
20	acg gcc ctc acc tac tac ctg gac atc acc aac ccg ccg cgt acc aac Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn 370 375 380				1152
25	gtg ctg tac gag ctg gcg cag tac gcc tcc gag ccc tcg gag cag gag Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu 385 390 395 400				1200
30	ctg ctg cgc aag atg gcc tcc tcc ggc gag ggc aag gag ctg tac Leu Leu Arg Lys Met Ala Ser Ser Gly Glu Gly Lys Glu Leu Tyr 405 410 415				1248
35	ctg agc tgg gtg gag gcc cgg agg cac atc ctg gcc atc ctg cag Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln 420 425 430				1296
40	gac tgc ccg tcc ctg cgg ccc atc gac cac ctg tgt gag ctg ctg Asp Cys Pro Ser Leu Arg Pro Ile Asp His Leu Cys Glu Leu Leu 435 440 445				1344
45	ccg cgc ctg cag gcc cgc tac tac tcc atc gcc tca tcc tcc aag gtc Pro Arg Leu Gln Ala Arg Tyr Tyr Ser Ile Ala Ser Ser Ser Lys Val 450 455 460				1392
50	cac ccc aac tct gtg cac atc tgt gcg gtg gtt gtg gag tac gag acc His Pro Asn Ser Val His Ile Cys Ala Val Val Val Glu Tyr Glu Thr 465 470 475 480				1440
55	aag gcc ggc cgc atc aac aag ggc gtg gcc acc aac tgg ctg cgg gcc Lys Ala Gly Arg Ile Asn Lys Gly Val Ala Thr Asn Trp Leu Arg Ala 485 490 495				1488
60	aag gag cct gcc ggg gag aac ggc ggc cgt gcg ctg gtg ccc atg ttc Lys Glu Pro Ala Gly Glu Asn Gly Gly Arg Ala Leu Val Pro Met Phe 500 505 510				1536
65	gtg cgc aag tcc cag ttc cgc ctg ccc ttc aag gcc acc acg cct gtc Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val 515 520 525				1584
70	atc atg gtg ggc ccc ggc acc ggg gtg gca ccc ttc ata ggc ttc atc Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Ile Gly Phe Ile 530 535 540				1632
75	cag gag cgg gcc tgg ctg cga cag cag ggc aag gag gtg ggg gag acg Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr 545 550 555 560				1680
80	ctg ctg tac tac ggc tgc cgc tcg gat gag gac tac ctg tac cgg Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg 565 570 575				1728
85	gag gag ctg gcg cag ttc cac agg gac ggt gcg ctc acc cag ctc aac Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn 580 585 590				1776
	gtg gcc ttc tcc cgg gag cag tcc cac aag gtc tac gtc cag cac ctg Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu 595 600 605				1824
	cta aag caa gac cga gag cac ctg tgg aag ttg atc gaa ggc ggt gcc Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala 610 615 620				1872
	cac atc tac gtc tgt ggg gat gca cgg aac atg gcc agg gat gtg cag His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln 625 630 635 640				1920
	aac acc ttc tac gac atc gtc gct gag ctc ggg gcc atg gag cac gcg Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala 645 650 655				1968

cag gcg gtg gac tac atc aag aaa ctg atg acc aag ggc cgc tac tcc Gln Ala Val Asp Tyr Ile Lys Lys Leu Met Thr Lys Gly Arg Tyr Ser 660 665 670	2016
ctg gac gtg tgg agc Leu Asp Val Trp Ser 675	2031

**Figure 3 - Nucleotide and protein sequence of Aspergillus
ochraceus oxidoreductase**

5	cttatttcgt ttaggaagag caccggcttc ggtgtccttc cttaccctct tattcttcct cttctgactc cctttttgtt attgatcgcc catctcggtg aacatggg atatcttcc ctctccccc cccgccccga ccctccttat ctttcctcc cgtccagcat ttagctcgcc atcgaattcg caatttccttc ctcgtgactc ttcatcgctg agcgtcctca tc atg gcg	60 120 180 238
	Met Ala 1	
10	caa ctc gat act ctc gat ttg gtc gtc ctg gtg gcg ctc ttg gtg ggt Gln Leu Asp Thr Leu Asp Leu Val Val Leu Val Ala Leu Leu Val Gly 5 10 15	286
15	agc gtg gcc tac ttc acc aag ggc acc tac tgg gcc gtc gcc aaa gac Ser Val Ala Tyr Phe Thr Lys Gly Thr Tyr Trp Ala Val Ala Lys Asp 20 25 30	334
20	cct tat gcc tcg gct ggt ccg gcg atg aat gga ggc gcc aag gcc ggc Pro Tyr Ala Ser Ala Gly Pro Ala Met Asn Gly Gly Ala Lys Ala Gly 35 40 45 50	382
25	aag act cgc gac att gtt cag aaa atg gac gaa act ggc aaa aac tgt Lys Thr Arg Asp Ile Val Gln Lys Met Asp Glu Thr Gly Lys Asn Cys 55 60 65	430
30	gtg att ttc tac ggc tcg caa acc ggt acc gct gag gac tac gcg tcc Val Ile Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Asp Tyr Ala Ser 70 75 80	478
35	aga ctg gcc aag gaa ggc tcc cag cga ttc ggt ctc aag acc atg gtg Arg Leu Ala Lys Glu Gly Ser Gln Arg Phe Gly Leu Lys Thr Met Val 85 90 95	526
40	gcc gat ctg gag gac tac gac tac gaa aac ctg gaa aag ttc ccc gag Ala Asp Leu Glu Asp Tyr Asp Tyr Glu Asn Leu Glu Lys Phe Pro Glu 100 105 110	574
45	gac aag gtt gtt ttc ttc gtt ctg gcc act tat ggc gag ggt gaa ccc Asp Lys Val Val Phe Phe Val Leu Ala Thr Tyr Gly Glu Gly Glu Pro 115 120 125 130	622
50	acg gat aat gcg gtt gaa ttc tac cag ttc gtc acg ggc gaa gat gct Thr Asp Asn Ala Val Glu Phe Tyr Gln Phe Val Thr Gly Glu Asp Ala 135 140 145	670
55	gct ttc gag agc ggc gct acc gcc gac gat aag cct ctg tct tct ctc Ala Phe Glu Ser Gly Ala Thr Ala Asp Asp Lys Pro Leu Ser Ser Leu 150 155 160	718
60	aag tat gtc acg ttt ggt ctg ggt aac aac acc tat gag cac tac aac Lys Tyr Val Thr Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn 165 170 175	766
65	gct atg gtt cgc aat gtg gac gcc gct ctc aca aag ttc ggc gcc caa Ala Met Val Arg Asn Val Asp Ala Ala Leu Thr Lys Phe Gly Ala Gln 180 185 190	814
70	cgc att ggc tct gct ggt gag ggt gac gac ggc gct ggt aca atg gaa Arg Ile Gly Ser Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu 195 200 205 210	862
75	gag gat ttc ctg gcc tgg aag gaa ccc atg tgg gct gcc ctt tct gag Glu Asp Phe Leu Ala Trp Lys Glu Pro Met Trp Ala Ala Leu Ser Glu 215 220 225	910
80	gcg atg aac ctg caa gag cgc gat gcg gtc tac gag ccg gtc ttc aat Ala Met Asn Leu Gln Glu Arg Asp Ala Val Tyr Glu Pro Val Phe Asn 230 235 240	958
85	gtc acc gag gac gag tcc ctg agc ccc gaa gat gag aac gtt tac ctc Val Thr Glu Asp Glu Ser Leu Ser Pro Glu Asp Glu Asn Val Tyr Leu 245 250 255	1006
90	ggt gag ccc act caa ggt cat ctc caa ggc gag ccc aag ggc ccg tac Gly Glu Pro Thr Gln Gly His Leu Gln Gly Glu Pro Lys Gly Pro Tyr 260 265 270	1054
95	tct gcg cac aac ccg ttc atc gct ccc atc tcc gaa tct cgt gaa ctg Ser Ala His Asn Pro Phe Ile Ala Pro Ile Ser Glu Ser Arg Glu Leu 275 280 285 290	1102

	ttc aac gtc aag gac cgc aac tgc ctg cac atg gaa atc agc atc gcc Phe Asn Val Lys Asp Arg Asn Cys Leu His Met Glu Ile Ser Ile Ala 295 300 305	1150
5	ggt agc aac ctc act tac cag act ggt gac cac atc gct gtt tgg ccc Gly Ser Asn Leu Thr Tyr Gln Thr Gly Asp His Ile Ala Val Trp Pro 310 315 320	1198
10	acc aac gcc ggt tcc gag gtc gat cgg ttc ctg cag gct ttt ggt ctc Thr Asn Ala Gly Ser Glu Val Asp Arg Phe Leu Gln Ala Phe Gly Leu 325 330 335	1246
15	gaa gga aag cgc cac tcc gtc atc aac att aag ggt atc gat gtg acc Glu Gly Lys Arg His Ser Val Ile Asn Ile Lys Gly Ile Asp Val Thr 340 345 350	1294
20	gtc aag gtt ccg att ccc act cct acg acc tat gac gcc gca gtt cgc Ala Lys Val Pro Ile Pro Thr Pro Thr Tyr Asp Ala Ala Val Arg 355 360 365 370	1342
25	tac tac ctg gaa gtc tgg gcc ccc gtt tcc cgt cag ttt gtc tcg act Tyr Tyr Leu Glu Val Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr 375 380 385	1390
30	ctc gct gcc ttt gcc cct gat gaa gcg acc aag gcg gag atc gtt cgt Leu Ala Ala Phe Ala Pro Asp Glu Ala Thr Lys Ala Glu Ile Val Arg 390 395 400	1438
35	ttg ggt ggc gac aag gac tat ttc cat gag aag att acc aac cga tgc Leu Gly Gly Asp Lys Asp Tyr Phe His Glu Lys Ile Thr Asn Arg Cys 405 410 415	1486
40	ttc aac atc gct cag gct ctc cag agc atc acg tcc aag cct ttc acc Phe Asn Ile Ala Gln Ala Leu Gln Ser Ile Thr Ser Lys Pro Phe Thr 420 425 430	1534
45	gcc gtc ccg ttc tcc ctg ctt atc gaa ggt atc acc aag ctt cag ccc Ala Val Pro Phe Ser Leu Leu Ile Glu Gly Ile Thr Lys Leu Gln Pro 435 440 445 450	1582
50	cgt tac tac tcg atc tcc tcg tct tcc ctg gtt cag aag gac aag att Arg Tyr Tyr Ser Ile Ser Ser Ser Leu Val Gln Lys Asp Lys Ile 455 460 465	1630
55	agc att acc gcc gtt gtg gag tcg gtt cgc ttg cct ggt gag gaa cac Ser Ile Thr Ala Val Val Glu Ser Val Arg Leu Pro Gly Glu Glu His 470 475 480	1678
60	att gtc aag ggt gtg acc acg aac tat ctt ctc gcg ctc aag gaa aag Ile Val Lys Gly Val Thr Thr Asn Tyr Leu Leu Ala Leu Lys Glu Lys 485 490 495	1726
65	caa aac ggc gag cct tcc cct gac ccg cac ggc ttg act tac tct atc Gln Asn Gly Glu Pro Ser Pro Asp Pro His Gly Leu Thr Tyr Ser Ile 500 505 510	1774
70	act gga ccc cgt aac aag tac gat ggc atc cat gtc ccc gtt cac gtc Thr Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val 515 520 525 530	1822
75	cgc cac tcg aac ttc aaa ttg ccc tcg gat ccc tcg cga cct gtg atc Arg His Ser Asn Phe Lys Leu Pro Ser Asp Pro Ser Arg Pro Val Ile 535 540 545	1870
80	atg gtt gga ccc ggt act ggt gtt gct cct ttc cgt ggg ttt atc cag Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Ile Gln 550 555 560	1918
85	gag cgt gct gcc ttg gcc gcg aag ggc gag aag gtc gga act acc ttg Glu Arg Ala Ala Leu Ala Lys Gly Glu Lys Val Gly Thr Thr Leu 565 570 575	1966
90	ctt ttc ttc ggc tgc cgt aag tcc gac gaa gat ttc ttg tac aag gat Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe Leu Tyr Lys Asp 580 585 590	2014
95	gaa tgg aag act ttt cag gag cag ctt ggc gac tcg ctc aag atc atc Glu Trp Lys Thr Phe Gln Glu Gln Leu Gly Asp Ser Leu Lys Ile Ile 595 600 605 610	2062
100	act gcc ttc tct cgt gaa tcg gct gag aaa gtc tac gtc cag cac agg Thr Ala Phe Ser Arg Glu Ser Ala Glu Lys Val Tyr Val Gln His Arg 615 620 625	2110
105	ctg cgt gag cat gcc gag ctg gtc agt gac ctg ctg aag cag cag aaa gcc	2158

	Leu Arg Glu His Ala Glu Leu Val Ser Asp Leu Leu Lys Gln Lys Ala	
	630 635 640	
5	act ttc tat gtt tgc ggt gac gct gcc aac atg gcc cgt gaa gtc aac	2206
	Thr Phe Tyr Val Cys Gly Asp Ala Ala Asn Met Ala Arg Glu Val Asn	
	645 650 655	
10	ctc gtg ctt ggg caa atc att gcc aag cag cgc ggt ctc cct gcc gag	2254
	Leu Val Leu Gly Gln Ile Ile Ala Lys Gln Arg Gly Leu Pro Ala Glu	
	660 665 670	
	aag ggc gag gag atg gtg aag cac atg cgc agc agc ggc agc tac cag	2302
	Lys Gly Glu Glu Met Val Lys His Met Arg Ser Ser Gly Ser Tyr Gln	
	675 680 685 690	
15	gac gat gtc tgg tcc taa aa	2322
	Asp Asp Val Trp Ser *	
	695	

Figure 4 - Amino acid homology alignment of *A. ochraceus* 11 alpha hydroxylase with the top 10 BLAST hits from GenBank

5	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	1 ---MANHSSYYHEFYKDHSHTVLILMSEKPVLPSLILGLTCAVLLC1QWLK--PQPLIM 1 -----MERLDIKSIIDPSATPFSYLVTAFLLA VVVVSLQGPRF-PKNIKH 1 -----LLFCFILSKTTKKGCONSOYS-NHDEL 1 -----MVMELHNHTPFYIYFITSILFIFVFKLVQRS--DSKTS-STCKLP 1 -----MPFFTGLLAIYHSLILDNPVQTLSTIVVLAAYA-LATLQ--PSDLPE 1 -----MSIFNMITSYAGQOLLPFYIAIFVFTLVPWAIRESWLELRK-GSVVPL 1 ---MTVDALTQPWHLLSLAWNDTQQHGSWFAPLVTTSAGLLCLLILCSSGR--RSDPV 1 ----- 1 -----MSKNSNMNSTSHETLFQQLVGLDRMPLMDVHWLIVYAFGAWLCSVIHVLSSSSTVVP 1 ----- 1 -----MALLIISLVI SIFTFFIYIILARRERKLREKIGLGSPEPH
15	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	56 VNGRKFGELSNVRAKRDFTFGARQLEKCLKMSPDKPFNIMGDVGELHILPPKYRVEERN 45 LNPKGPLEFSDTPKKEVYGSRQVIANWFKANPNKPCVTSDFGEATVLLPPRMANEIKN 28 PGPPQIPILGNALQSGCH-THEI ERLAKKYGPLMHLK--I GEVSTVVAASSPQIAEDEIFR 45 PGPRTLPLIGNIQIVGSLPVHYYKLNLDKYGPLMHLK--I GEVSNLIVTSPPEMAOFIMK 46 LNPAPKPFETNRRVHEEVENSKSLEAARGRELHGHEPYILMSEWGSILVLPPECADEFRN 48 ANPPD-SLFGTGTTRSEPVKLSREIATKARSLSLFPNEPPFLITWGEVLLUPPDFADEFRN 56 FNPKTWWELTTMRAARDEDANAPSWESWFQSQ-DKPIFIVDGSYCTLPSSMADEFNK 61 VVGYRSVFEPTWLLSLRIVWEGGSQGQYNKFKDSIFQVRKLGTDPPNYIDDK 1 ----- 1 ----- 43 WFLGNLKQTAERELCLGDDANWFNELHEQYGETFGIY-YGSQMN SNEKDIKEIFI
20	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	116 NEKISPTMAA--FKWFWYAHLPFGEG--FREGTNESIILKLVARHOLT--QQT1ITGAI 105 DDRSPTTRWT-YKAFTGHLPGFEG--FGEASRESIIVQEVIMRDLT--KYNKVEPEA 86 THDLFADRPSNLESEPIVSYDLSDMVVSPYGNWQQRSMMEILSQSSQSFRSIRE 104 THDLSNSDRP-DFVLSLIVSYNGSGIVFSQHGDYWLQKCTVETLTARQOSFRSIRE 106 DPRDDEPTP--TDDSGYIPGFDA--LN-ADPNTTIVVTKYLT--KALNKETAPS 107 DPRSBSKAA--MQDNHAGIPGFET--VALVGREDQLQXAVRKQLI--KHSANIEEPS 115 MKECMYKFLG-TDFSHLPGFEG--FKEVTRDAILTKVVMNQFO-TQAPKVKPVA 1 ----- 1 ----- 121 LS---QDKTRSVEPFINDFAGQYT--RGMVFLQSDLQNQVVIQQRLI--PKIVSFTKVMK 1 ----- 102 KNFSNFSDRS--VPSIYEANQLTASLLMNSYSSGIVHTRSAIAPIFS-TGKKAQPTIN
25	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	170 EECALVWKDQYTDSP--WHD-TAKDANAKLARLTSRVLGKEHCPNPOWLRT--STYA 159 QETSMIAEANLPKAANGWSTNRSKLPIVARISSRVFGEELCRNEEWLKV--QQYT 146 EEVLNFIKSIG--SKEG-TRIN-SKEISLILYGFTRRAFGEKKNITFETRLDQLTK 163 EEEVAELKKIATASEEGGSIFNTQSISYMTFGAAARAFGKKSRYCQVFSNMHKQLM 156 HEASIAMKAALGDDP-DWRETPARDLQLVARMSTRTVFLGEECNMQDWQTS-SOYA 161 RESTLAISLNFGETT--WRAKPKAIDTARISSRILYLGDOIICHNEAWLK--KTYT 169 NEASGIFTDFGDSN--WHTVPMYNOCDLVTRTVFIMVCSKIAAENEWLLDIA-KHHA 17 MTKTSFRWPRTS--KNSSSISYDMTRTVALSCRAFVGLPCEEEGWLQAS-IGYT 50 173 EELDYATKEMPDMDKNDWVWEDLSSIMVRLISRISARVELGPEHCKNQEWLIT-AEYS 1 ----- 159 SKVDLFIDIREKAS--SGQKWDYDDFQGLTLDDIGCAFIDSNCRDRNDIFYHPVT
40	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	227 VIAFRAVEELRIMP-SWLRPVQWMEHCTQSRAIYQENRDPINPDLER-RPREEK--AEA 218 EDGFGAAEDLRLWP-AALRPVHWFPSCQRARADIVARSIDDPVIEKK-RRQEK--AAN 202 AVAEPIIADFPSSL-KFLQLSTS KYKIEKIHQFDVIVETIKGHKKEKINKPLS--QEN 223 EGGFSVADLYPSS-RFOMMGATG-KLEKVHRVTDVVLQDI-DEHK--NRRNRS--SEE 213 ALAFGVGDKLRIMP-RDTRP-VHWFPSCWEIIRRSHRCRQIITFVYHK-RASL--GTT 218 TNFYTASTNLRMFP-RSRPLAHWEPECRKLROERKDAIGITPTEER-RRELR--RAA 226 VTMIAIQARQLRIMP-VLRLPVAHWLFPQGAKLRAQYRRAQEDPTEQE-RRAER--DAC 70 YQCVSIRDQLFTEAS-PVLRPVGEPYPSVRSVRRHFRFAETMAPLSQALQDEMOHRAD 232 ESLFITGFILRWP-HILRPFIAPILPSYRTLRLNWSGRRGTDGDTR--SOQ-- 1 ----- CAA57874 CAA91268 217 VKITINNFTYFHSSPGTFHFESTQIHTTGRCRNSTCRRTCKCGFRODKAKFCSDYE
45	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	
50	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	
55	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	
60	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	
65	CAA75565 CAB91316 CAB56503 AAB94588 dMON45624 CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	

5	CAA75565 CAB91316 CAB56503 AAB94588 pMON45624	283 ERTGEKV-TYNDLAEWLDLAREK--EVGYDPACAOVSLSVAA--IHTSTDFFTQVMFDI 274 ---GGKA-EHDDAEMFERTA--K-CKYDPAMAOVLSVA--IHTTSIDLTCQVMTNL 259 G--EKKE-DLVDVLNIQRRNDFE--SPLGDKNKAIFNFSAGTETSSTTDWAMCEM 276 R--EAVE-DLVDVLKFQKES--E-FRLTDDNKAVIDFIGGETTSVNEWMSL 269 DEOCKPL-MFDDSIEMFEREL---SPNHDAAVEKQVTLSTVMA--IHTTSIDLQAMSDL CAA75566 AAD34552 CAA75567 CAA76703 CAA57874 CAA91268	274 IAAQPLPVFHADWSEQEAAAGTASFDPVIFQTLSSL--IHTTYDILQQTMDL 282 RAKGIEPPRVLSSQWFEDTAK--CKWYDAAGQALANDFAG--IYGTSIDLIGGIVD 129 TLLDQTEGRGTFESWLLRHLPL-EELRTPEQVGDOMLYSFA--IHTTMA-TKVMWL 282 --GDGN--EILISMMRDAATGEE-KQIDMIAORMILSAS--IHTTAMWTHAMYDL 44 --LEDPPMTMLDHLNSGRNHEHIA---DDVELQLPHOMTLIAVS--TVTTFSSTTQNYDL 277 RRGEGGSDSVLKLNNREDDKS-KPMTKQEVENCFVFLLAGYETTSTATYCSYLL
10	CAA75565 CAA57874 CAA91268	338 AQPEDIEPLRHEIAVEGKQG--WKSNSLYNLKLMDSVKEESQRK--P----- 324 MNQPFIAPLREMIQVSECG--SKTSLYNLKLDSDVKEESQRK--P----- 314 LNEPTVKKAEDEVRKVNEEGN--VDETKHOLKYLQVKEELRRE--P----- 329 LNPRYMEEAQAQEVRRVYDSDKY--VDETEHQIYLKSIKEELMRE--P----- 321 AQPENKQAEQAREVVRVYSTEGL--LSKVSILHSLKLMDSVKEESQRK--P----- 332 GEPPEYIEPLRQEVQVQFREEG--WKTDFKMKLKDSDVKEESQRK--P----- 336 VPHPHIEPLRDETRTVLGQGG--TPASLYKLKLLDSDVKEESQRK--P----- 336 VPHPHIEPLRDETRTVLGQGG--TPASLYKLKLLDSDVKEESQRK--P----- 186 VPHPEYIEPLRIMODVFGPDAVSPDICINCAEGLRHLKLDSEFREVORWC--P----- 333 CACPEYIEPLRQEVKSVWAGSG--WKTDFNRFHKLDSFVKEESQRK--P----- 96 VPHPEYITILKEEVESVPRDPNGN--WKTDSVAMDKLDSFVKEESQRK--P----- CAA91268 336 SKYENQOKLVEEIMEAKENG--LTYDSHNWKYLDCCVYKEELRFY--P-----	338 AQPEDIEPLRHEIAVEGKQG--WKSNSLYNLKLMDSVKEESQRK--P----- 324 MNQPFIAPLREMIQVSECG--SKTSLYNLKLDSDVKEESQRK--P----- 314 LNEPTVKKAEDEVRKVNEEGN--VDETKHOLKYLQVKEELRRE--P----- 329 LNPRYMEEAQAQEVRRVYDSDKY--VDETEHQIYLKSIKEELMRE--P----- 321 AQPENKQAEQAREVVRVYSTEGL--LSKVSILHSLKLMDSVKEESQRK--P----- 332 GEPPEYIEPLRQEVQVQFREEG--WKTDFKMKLKDSDVKEESQRK--P----- 336 VPHPHIEPLRDETRTVLGQGG--TPASLYKLKLLDSDVKEESQRK--P----- 336 VPHPHIEPLRDETRTVLGQGG--TPASLYKLKLLDSDVKEESQRK--P----- 186 VPHPEYIEPLRIMODVFGPDAVSPDICINCAEGLRHLKLDSEFREVORWC--P----- 333 CACPEYIEPLRQEVKSVWAGSG--WKTDFNRFHKLDSFVKEESQRK--P----- 96 VPHPEYITILKEEVESVPRDPNGN--WKTDSVAMDKLDSFVKEESQRK--P----- CAA91268 336 SKYENQOKLVEEIMEAKENG--LTYDSHNWKYLDCCVYKEELRFY--P-----
15	CAA75565 CAB91316 CAB56503 AAB94588 pMON45624	384 -----IAIASMRRFTTHNKLSDCVIIPKNNKLTIVSAQHW-----DPEYIK 370 -----TGVASMRRYAEKDMTLSDGTFIPKGGEAVVASBQHWW-----NSEVNEO 361 -----PVELLPRECREOCKK--GYTPSKTSPMIVNAWAGR-----DPNYVIE 376 -----PVPLLVPVRVSRCQEN-GYEIPSKTRTINNAWAGR-----NPKYVGE 367 -----TLLGSFRRQATNDKLLKSGFVIIKKGTRVYD--DSTHWM-----NPEYITD CAA75566 378 -----GSIVTMRBYVTEDTLSSOLTKKGTIVNDVNRD-----DPKIMDN 382 -----VECA-MRSYALQDMTFSNGTFIPKCELIVAAVADRM-----NPEVVPD 35 378 -----STVFPSPSRVVMKSYTLSNCIKLQGIGSIAFPAAAHMSEETPTFSPDFSS CAA75567 238 -----VFLLEFNRIYHQSYTLSDCTNIPSGTKIAVPEAALQ-----DSAHPVG CAA76703 379 -----VFLLEFNRIYHQSYTLSDCTNIPSGTKIAVPEAALQ-----DSAHPVG CAA57874 152 KNYKLCESLTGHSN-PTRTIADYKLDPCTFVPKGTKEINTCSHK-----DHKLHEN CAA91268 382 -----PHFSFIRRLCREDIIR-GQFYPKGAIWVCLPENHR-----NPENHDS	384 -----IAIASMRRFTTHNKLSDCVIIPKNNKLTIVSAQHW-----DPEYIK 370 -----TGVASMRRYAEKDMTLSDGTFIPKGGEAVVASBQHWW-----NSEVNEO 361 -----PVELLPRECREOCKK--GYTPSKTSPMIVNAWAGR-----DPNYVIE 376 -----PVPLLVPVRVSRCQEN-GYEIPSKTRTINNAWAGR-----NPKYVGE 367 -----TLLGSFRRQATNDKLLKSGFVIIKKGTRVYD--DSTHWM-----NPEYITD CAA75566 378 -----GSIVTMRBYVTEDTLSSOLTKKGTIVNDVNRD-----DPKIMDN 382 -----VECA-MRSYALQDMTFSNGTFIPKCELIVAAVADRM-----NPEVVPD 35 378 -----STVFPSPSRVVMKSYTLSNCIKLQGIGSIAFPAAAHMSEETPTFSPDFSS CAA75567 238 -----VFLLEFNRIYHQSYTLSDCTNIPSGTKIAVPEAALQ-----DSAHPVG CAA76703 379 -----VFLLEFNRIYHQSYTLSDCTNIPSGTKIAVPEAALQ-----DSAHPVG CAA57874 152 KNYKLCESLTGHSN-PTRTIADYKLDPCTFVPKGTKEINTCSHK-----DHKLHEN CAA91268 382 -----PHFSFIRRLCREDIIR-GQFYPKGAIWVCLPENHR-----NPENHDS
20	CAA75565 CAA57874 CAA91268	427 PLK-----FDGRRFFNMRREP--GKESKAQLVSATP-----FCYGLHACPGRFFASEEIK 413 AEK-----MDGRFLRMRRETGPAGKENVAQLVSTAP-----FCGHCOHACPGRFFAANEIK 404 PEK-----FNPDRFLES-----K--VDFKGNSFEYD-PFGGGRRICPGCITFALANIE 419 TES-----FKPBRFLNS-----S---IDFRGIDEF-----PFGACRRICPGCITFAIPNTE 410 PLQ-----DGVRFNFNKRQTP--GEDKNALLVSTSANHAGFCGHGVHACPGRFFASNEIK 421 PEV-----YNPYRFDYDNESEA--GKDHDGAOLVSTGSNHHMGFCGHQOHSCPGRFFAANEIK 425 PAK-----MPEYRMRLEDPD--KAFAASQALENNGCHGFCGHPRACPGRFFASKEIKM 289 FENPSPRIFDGHRYLNRSIK--GQGSQHQAA-TGPEYIIFNFGKACPGRFFAISEIKM CAA76703 423 PTP--PTEFDGHRYSKRSDS--NYAOKYLFMSMTDSNSNMAFGCYCKYACPGRFFASNEIK CAA57874 205 PEQ-----FDQLRFHKWKRAP--GKEKRYMYSSESGTEDLSHSGGRHACPGHGLSAINIK CAA91268 425 PPE-----FHPERFENWE-----E-----KSSSLKWPFGVGPYCVGMRAEEMEFT	427 PLK-----FDGRRFFNMRREP--GKESKAQLVSATP-----FCYGLHACPGRFFASEEIK 413 AEK-----MDGRFLRMRRETGPAGKENVAQLVSTAP-----FCGHCOHACPGRFFAANEIK 404 PEK-----FNPDRFLES-----K--VDFKGNSFEYD-PFGGGRRICPGCITFALANIE 419 TES-----FKPBRFLNS-----S---IDFRGIDEF-----PFGACRRICPGCITFAIPNTE 410 PLQ-----DGVRFNFNKRQTP--GEDKNALLVSTSANHAGFCGHGVHACPGRFFASNEIK 421 PEV-----YNPYRFDYDNESEA--GKDHDGAOLVSTGSNHHMGFCGHQOHSCPGRFFAANEIK 425 PAK-----MPEYRMRLEDPD--KAFAASQALENNGCHGFCGHPRACPGRFFASKEIKM 289 FENPSPRIFDGHRYLNRSIK--GQGSQHQAA-TGPEYIIFNFGKACPGRFFAISEIKM CAA76703 423 PTP--PTEFDGHRYSKRSDS--NYAOKYLFMSMTDSNSNMAFGCYCKYACPGRFFASNEIK CAA57874 205 PEQ-----FDQLRFHKWKRAP--GKEKRYMYSSESGTEDLSHSGGRHACPGHGLSAINIK CAA91268 425 PPE-----FHPERFENWE-----E-----KSSSLKWPFGVGPYCVGMRAEEMEFT
25	CAA75565 CAB91316 CAB56503 AAB94588 pMON45624	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----
30	CAA75565 CAA57874 CAA91268	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----
35	CAA75565 CAA57874 CAA91268	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----
40	CAA75565 CAB91316 CAB56503 AAB94588 pMON45624	427 PLK-----FDGRRFFNMRREP--GKESKAQLVSATP-----FCYGLHACPGRFFASEEIK 413 AEK-----MDGRFLRMRRETGPAGKENVAQLVSTAP-----FCGHCOHACPGRFFAANEIK 404 PEK-----FNPDRFLES-----K--VDFKGNSFEYD-PFGGGRRICPGCITFALANIE 419 TES-----FKPBRFLNS-----S---IDFRGIDEF-----PFGACRRICPGCITFAIPNTE 410 PLQ-----DGVRFNFNKRQTP--GEDKNALLVSTSANHAGFCGHGVHACPGRFFASNEIK 421 PEV-----YNPYRFDYDNESEA--GKDHDGAOLVSTGSNHHMGFCGHQOHSCPGRFFAANEIK 425 PAK-----MPEYRMRLEDPD--KAFAASQALENNGCHGFCGHPRACPGRFFASKEIKM 289 FENPSPRIFDGHRYLNRSIK--GQGSQHQAA-TGPEYIIFNFGKACPGRFFAISEIKM CAA76703 423 PTP--PTEFDGHRYSKRSDS--NYAOKYLFMSMTDSNSNMAFGCYCKYACPGRFFASNEIK CAA57874 205 PEQ-----FDQLRFHKWKRAP--GKEKRYMYSSESGTEDLSHSGGRHACPGHGLSAINIK CAA91268 425 PPE-----FHPERFENWE-----E-----KSSSLKWPFGVGPYCVGMRAEEMEFT	427 PLK-----FDGRRFFNMRREP--GKESKAQLVSATP-----FCYGLHACPGRFFASEEIK 413 AEK-----MDGRFLRMRRETGPAGKENVAQLVSTAP-----FCGHCOHACPGRFFAANEIK 404 PEK-----FNPDRFLES-----K--VDFKGNSFEYD-PFGGGRRICPGCITFALANIE 419 TES-----FKPBRFLNS-----S---IDFRGIDEF-----PFGACRRICPGCITFAIPNTE 410 PLQ-----DGVRFNFNKRQTP--GEDKNALLVSTSANHAGFCGHGVHACPGRFFASNEIK 421 PEV-----YNPYRFDYDNESEA--GKDHDGAOLVSTGSNHHMGFCGHQOHSCPGRFFAANEIK 425 PAK-----MPEYRMRLEDPD--KAFAASQALENNGCHGFCGHPRACPGRFFASKEIKM 289 FENPSPRIFDGHRYLNRSIK--GQGSQHQAA-TGPEYIIFNFGKACPGRFFAISEIKM CAA76703 423 PTP--PTEFDGHRYSKRSDS--NYAOKYLFMSMTDSNSNMAFGCYCKYACPGRFFASNEIK CAA57874 205 PEQ-----FDQLRFHKWKRAP--GKEKRYMYSSESGTEDLSHSGGRHACPGHGLSAINIK CAA91268 425 PPE-----FHPERFENWE-----E-----KSSSLKWPFGVGPYCVGMRAEEMEFT
45	CAA75565 CAA57874 CAA91268	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----
50	CAA75565 CAA57874 CAA91268	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----
55	CAA75565 CAA57874 CAA91268	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----
60	CAA75565 CAA57874 CAA91268	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----	480 AISHLILKYDEKPKV-----EGSSMEPRKYCINANANPATAKLSVRRK-EIHA----- 468 AIVHLLNYWNLIP-----EGSDPKIRTGFSGVDPSLAEYGRQ-PFEL----- 449 PIAQLLFEDWOS-----NTEKLNMK-E-SRGVTVREDDLYLTPVNFS-SSSPA----- 464 PIAQLLYHEDWKIPNPKMKNEELDMTE-SNGTTRQNDLCLIPITR-----P 463 AICHLILNYWNLIP-----DGFKPQPLNIGTYLADPNTMILRPRK-AEDMASLT 474 AICHLILNYWNLIP-----PDTETKPDTRGMIAKSSPVTDLILKRRRESVE-DLEAI-- 478 MIAELLLRYDWKLV-----PDEPLQYYRHFSVRIHPTTAKMURRRD-EDRLPGSL 347 IELIELLARYDNL-----DGKPGPELMRVCTETRLDTKAGEMERR 479 TIAILLQDNLKIP-----DGKGRPRNITIDSDIIPDRAFLCNRKS--ERDE----- 258 IMAELLLNYLILKLP-----DGLSRPKNIEFEMLASLNACANA----- CAA91268 468 TIVKULDTILKQF-----EGEADLIPDCNGVTPNDPV-EHPRN-----
65	CAA75565 CAB91316 CAB56503 AAB94588 pMON45624	(SEQ ID NO: 27) (SEQ ID NO: 28) (SEQ ID NO: 29) (SEQ ID NO: 30) (SEQ ID NO: 02) (SEQ ID NO: 31) (SEQ ID NO: 32)	(SEQ ID NO: 27) (SEQ ID NO: 28) (SEQ ID NO: 29) (SEQ ID NO: 30) (SEQ ID NO: 02) (SEQ ID NO: 31) (SEQ ID NO: 32)
70	CAA75565 CAA57874 CAA91268	(SEQ ID NO: 33) (SEQ ID NO: 34) (SEQ ID NO: 35)	(SEQ ID NO: 33) (SEQ ID NO: 34) (SEQ ID NO: 35)
75	CAA91268	(SEQ ID NO: 36)	(SEQ ID NO: 36)

**Figure 5 - Phylogenetic tree showing the relatedness of
Aspergillus ochraceus 11 alpha hydroxylase to the top 10
BLAST hits from GenBank**

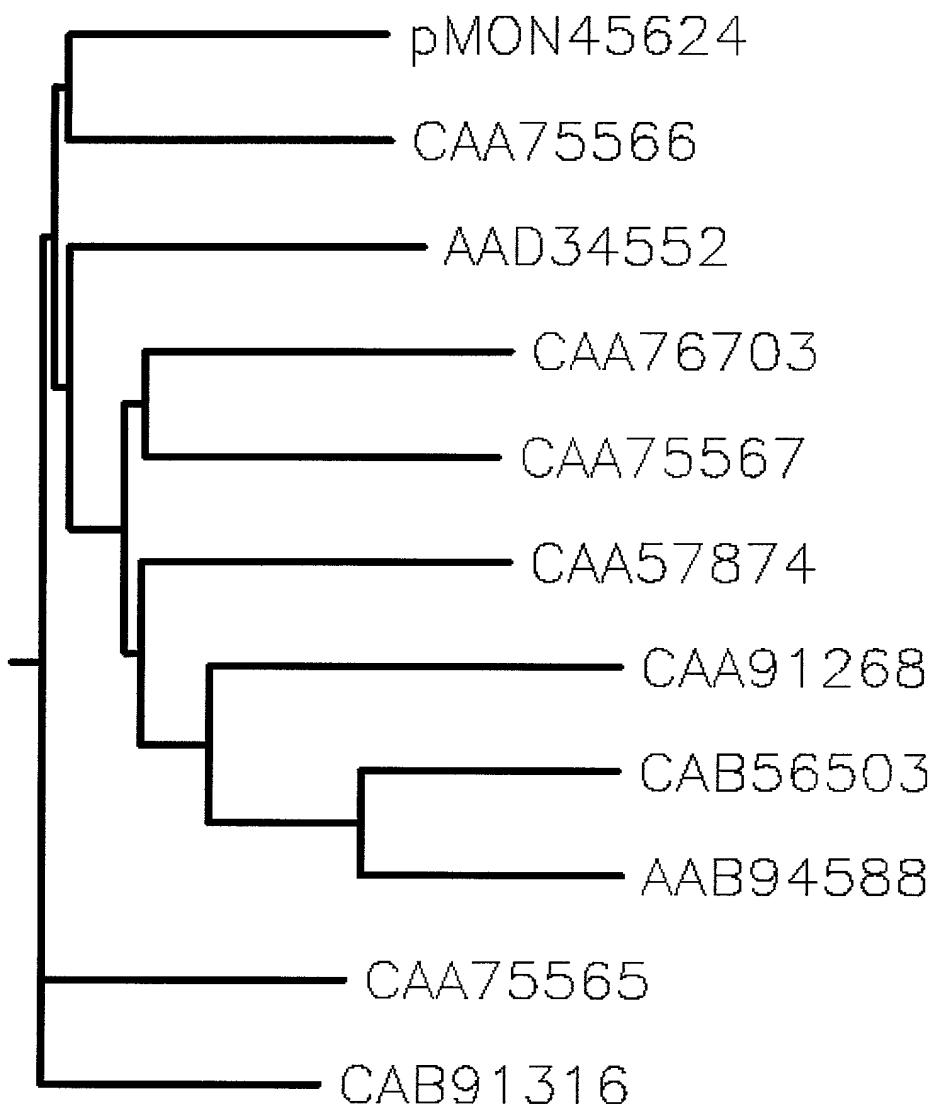


Figure 6 – Percent homology of *Aspergillus ochraceus* 11 alpha hydroxylase to the top 10 BLAST hits from GenBank

Accession Number	Species	% ID to 11a OH
CAB91316	<i>Neurospora crassa</i>	40
CAA76565	<i>Gibberella fujikuroi</i>	37
CAA75566	<i>Gibberella fujikuroi</i>	37
AAD34552	<i>Aspergillus terreus]</i>	29
CAA75567	<i>Gibberella fujikuroi</i>	24
CAA57874	<i>Fusarium oxysporum</i>	24
CAA76703	<i>Gibberella fujikuroi</i>	23
CAB56503	<i>Catharanthus roseus</i>	14
AAB94588	<i>Glycine max</i>	14
CAA91268	<i>Caenorhabditis elegans</i>	12

Figure 7 – Amino acid homology alignment of *A. ochraceus* and human oxidoreductase to NADPH cytochrome P450 reductases from *A. niger*, mouse, and *S. cerevisiae*

5	PMON45605	1	MGDSHVDTSSTVSEAVAEEVSLRSMTDMILFSLIVGELTYWFLFRKKKEEVPEFTKIQTL	human	1	MGDSHVDTSSTVSEAVAEEVSLRSMTDMILFSLIVGELTYWFLFRKKKEEVPEFTKIQTL
	mouse	1	MGDSHVDTSSTVSEAVAEEVSLRSMTDMILFSLIVGELTYWFLFRKKKEEVPEFTKIQTL		1	MGDSHEDTSATIPEAVAEEVSLESTTDINLFSLIVGELTYWFLFRKKKEEVPEFSKIQTT
	pMON45632	1	MGDSHEDTSATIPEAVAEEVSLESTTDINLFSLIVGELTYWFLFRKKKEEVPEFSKIQTT		1	--MAQDTLIDLVVLLVALLVGSVAYFTKG-----TYWAVAKDPYA--SAGPAVNGG
	niger	1	--MAQDTLIDLVVLLVALLVGSVAYFTKG-----TYWAVAKTRMP--LPAPRNGA		1	--MAQDTLIDLVVLLVALLVGSVAYFTKG-----TYWAVAKTRMP--LPAPRNGA
10	yeast	1	--MAQDTLIDLVVLLVALLVGSVAYFTKG-----TYWAVAKTRMP--LPAPRNGA		1	-MPFGIDNIDPTVLAGLVLVAVLILYVKRN-----SIKEILMSDDG-----DT-
	PMON45605	61	TSSVREESSFVEKMKKTGRNIIIVFGSQTGTAAEEFANRLSKD-AHRYGMRGMSADPEEYDL	human	61	TSSVREESSFVEKMKKTGRNIIIVFGSQTGTAAEEFANRLSKD-AHRYGMRGMSADPEEYDL
	mouse	61	TSSVREESSFVEKMKKTGRNIIIVFGSQTGTAAEEFANRLSKD-AHRYGMRGMSADPEEYDL		61	APPVKESSFVEKMKKTGRNIIIVFGSQTGTAAEEFANRLSKD-AHRYGMRGMSADPEEYDL
15	pMON45632	47	AKAGKTRDIVEKMDETGENCVIFYFGSQTGTAAEDVASYSLRAKEGSOREGEKTMVADLEEDYD		47	AKAGKTRNTEKMEETGENCVIFYFGSQTGTAAEDVASYSLRAKEGSOREGEKTMVADLEEDYD
	niger	47	AKAGKTRNTEKMEETGENCVIFYFGSQTGTAAEDVASYSLRAKEGSOREGEKTMVADLEEDYD		42	AVSSGNRDIASVTEENNKNYILYISQTGTAAEDVASYSLRAKEGSOREGEKTMVADLEEDYD
20	PMON45605	120	ADLSSLPEIDNALVVFCMATYGEGDPTDNAQDFYDNLQ-----ET-----DVDSLGMKE	human	120	ADLSSLPEIDNALVVFCMATYGEGDPTDNAQDFYDNLQ-----ET-----DVDSLGMKE
	mouse	120	ADLSSLPEIDKSLLVVFCMATYGEGDPTDNAQDFYDNLQ-----ET-----DVDSLGMKE		120	ADLSSLPEIDKSLLVVFCMATYGEGDPTDNAQDFYDNLQ-----ET-----DVDSLGMKE
	pMON45632	107	ENLEKPFEDK-WVFPVATYGEGLPTDNAVVFYQEVFTGEDAAFESGATADDKPLSSKKY		107	ENLDQFPE-DK-WAFFVATYGEGLPTDNAVVFYQEVFTGEDAAFESGATADDKPLSSKKY
25	niger	107	ENLDQFPE-DK-WAFFVATYGEGLPTDNAVVFYQEVFTGEDAAFESGATADDKPLSSKKY		102	ESLNDLTPV-----VSIFESTYGEGLFPDCAVNFEDPFCN-----APAG-----ALSNEY
	yeast	102	ESLNDLTPV-----VSIFESTYGEGLFPDCAVNFEDPFCN-----APAG-----ALSNEY			
30	PMON45605	169	AVFGLGNKTYEHFNAMGKYVVDKRLLEQLGAORIFELGLGDD-DGNLEEDFTTWREQFWPAV	human	169	AVFGLGNKTYEHFNAMGKYVVDKRLLEQLGAORIFELGLGDD-DGNLEEDFTTWREQFWPAV
	mouse	169	AVFGLGNKTYEHFNAMGKYVVDKRLLEQLGAORIFELGLGDD-DGNLEEDFTTWREQFWPAV		169	AVFGLGNKTYEHFNAMGKYVVDKRLLEQLGAORIFELGLGDD-DGNLEEDFTTWREQFWPAV
	pMON45632	165	VTFLGLGNNTYEHYNAMVRNVDAAALTKFGAORIGSAGEGDDGAGTMEEDFTIAKEPMIAAL		165	VTFLGLGNNTYEHYNAMVRNVDAAALTKFGAORIGSAGEGDDGAGTMEEDFTIAKEPMIAAL
	niger	164	VAFLGLGNNTYEHYNAMVRNVDAAAFKLGORIGSAGEGDDGAGTMEEDFTIAKEPMIAAL		164	VAFLGLGNNTYEHYNAMVRNVDAAAFKLGORIGSAGEGDDGAGTMEEDFTIAKEPMIAAL
	yeast	148	NMFLGLNSTYEFFNCAAKKAELSAAGAIREGKLGEEADDGAGTTDEDYAWKDSILEV		148	NMFLGLNSTYEFFNCAAKKAELSAAGAIREGKLGEEADDGAGTTDEDYAWKDSILEV
35	PMON45605	228	CEHFGFEATGEESSIROYELVVHED-----DAAKVYMGEMGRLKSY-----ENOKP	human	228	CEHFGFEATGEESSIROYELVVHED-----DAAKVYMGEMGRLKSY-----ENOKP
	mouse	228	CEHFGFEATGEESSIROYELVVHED-----DAAKVYMGEMGRLKSY-----ENOKP		228	CEFFGFEATGEESSIROYELVVHED-----MDTAKVYMGEMGRLKSY-----ENOKP
40	pMON45632	225	SEAMNIEC---ERDAVYEPVFNVTEDESLSPEDENVYLGEPTQHQLQ-----GEPKG		225	SEAMNIEC---ERDAVYEPVFNVTEDESLSPEDENVYLGEPTQHQLQ-----GEPKG
	niger	224	SESMDEIE---EREAIVEPVFCVTENESLSPEDETVYLGEPTQHQLQ-----GEPKG		224	SESMDEIE---EREAIVEPVFCVTENESLSPEDETVYLGEPTQHQLQ-----GEPKG
	yeast	208	KDELHED---EQEAKFTSDFQYTVLNL-----EITDMSLGEPSAHYLPQHQLRNRAQGQLG		208	KDELHED---EQEAKFTSDFQYTVLNL-----EITDMSLGEPSAHYLPQHQLRNRAQGQLG
45	PMON45605	275	PFDAKNPFLAAVTTNRKLNQGTERHIMHLELDISDSKIRYE SGDHVAVMPANDSALVNQL	human	275	PFDAKNPFLAAVTTNRKLNQGTERHIMHLELDISDSKIRYE SGDHVAVMPANDSALVNQL
	mouse	275	PFDAKNPFLAAVTTNRKLNQGTERHIMHLELDISDSKIRYE SGDHVAVMPANDSALVNQL		275	PFDAKNPFLAAVTTNRKLNQGTERHIMHLELDISDSKIRYE SGDHVAVMPANDSALVNQL
	pMON45632	273	PYSANNPFLAPAESRELFNVKDRNCHMEISIAGSNITYQIGDIAVWPTNAGSEVERF		273	PYSANNPFLAPAESRELFNVKDRNCHMEISIAGSNITYQIGDIAVWPTNAGSEVERF
	niger	272	PYSANNPFLAPAESRELFNVKDRNCHMEISIAGSNITYQIGDIAVWPTNAGSEVERF		272	PYSANNPFLAPAESRELFNVKDRNCHMEISIAGSNITYQIGDIAVWPTNAGSEVERF
50	yeast	262	PFDSLSPYFLAPVKSEELFSSNDRNCIHSFDSGSMNIKYSQGDHVAVWPSNPLEKVEQF		262	PFDSLSPYFLAPVKSEELFSSNDRNCIHSFDSGSMNIKYSQGDHVAVWPSNPLEKVEQF
	PMON45605	335	GKILGAD--LDVVMMSLNNLDEESENKKHPFPCCPTSYRITALTYLDTINPPRTNVLYELAQY	human	335	GKILGAD--LDVVMMSLNNLDEESENKKHPFPCCPTSYRITALTYLDTINPPRTNVLYELAQY
	mouse	335	GKILGAD--LDVVMMSLNNLDEESENKKHPFPCCPTSYRITALTYLDTINPPRTNVLYELAQY		335	GKILGAD--LDVVMMSLNNLDEESENKKHPFPCCPTSYRITALTYLDTINPPRTNVLYELAQY
	pMON45632	333	LQAFGLGKRHSVNLNGKGD-----VTAKVPPIPTPTVDAAVRYLEVCAPVSRQFATLAAF		333	LQAFGLGKRHSVNLNGKGD-----VTAKVPPIPTPTVDAAVRYLEVCAPVSRQFATLAAF
	niger	332	LQAFGLGKRHSVNLNGKGD-----VTAKVPPIPTPTVDAAVRYLEVCAPVSRQFATLAAF		332	LQAFGLGKRHSVNLNGKGD-----VTAKVPPIPTPTVDAAVRYLEVCAPVSRQFATLAAF
	yeast	322	LSLFNLD--PTEFDIKPLD--PTWKVPFPTPTVIGAAKHYLTTGPVSRQFATLAAF		322	LSLFNLD--PTEFDIKPLD--PTWKVPFPTPTVIGAAKHYLTTGPVSRQFATLAAF
60	PMON45605	393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDCP-SLRPPIDHLCELLPR	human	393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDCP-SLRPPIDHLCELLPR
	mouse	393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDCP-SLRPPIDHLCELLPR		393	AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDCP-SLRPPIDHLCELLPR
	pMON45632	391	APDEAKAEVRLCQDKDYFHEKFTNRCFNIAQ---ALQSIITSKP-FTAVPFSLLIEGTTK		391	APDEAKAEVRLCQDKDYFHEKFTNRCFNIAQ---ALQSIITSKP-FTAVPFSLLIEGTTK
	niger	390	APMRKARORLICWVVAQG-LFPFEGHQPMIQAQ---ALQSIITSKP-FSAVPFSLLIEGTTK		390	APMRKARORLICWVVAQG-LFPFEGHQPMIQAQ---ALQSIITSKP-FSAVPFSLLIEGTTK
65	yeast	378	APNADVKEKLTLLSKDKDQFVETTSKTFNID--ALKYLSDGAKWDNVPMOFIVESVPO		378	APNADVKEKLTLLSKDKDQFVETTSKTFNID--ALKYLSDGAKWDNVPMOFIVESVPO
70	PMON45605	451	LOARYYSIASSSKVHPNSVHICAVVVEYETK-----AGRINKGVATNWLRAKEP--AGE--	human	451	LOARYYSIASSSKVHPNSVHICAVVVEYETK-----AGRINKGVATNWLRAKEP--AGE--
	mouse	451	LOARYYSIASSSKVHPNSVHICAVVVEYETK-----AGRINKGVATNWLRAKEP--AGE--		451	LOARYYSIASSSKVHPNSVHICAVVVEYETK-----AGRINKGVATNWLRAKEP--AGE--
	pMON45632	448	LOPRYYSISSSSLVQKDKSITAVVESVRLP---GEEIVKGVITTNLLALKQKQNGEPS		448	LOPRYYSISSSSLVQKDKSITAVVESVRLP---GEEIVKGVITTNLLALKQKQNGEPS
	niger	446	LOPRYYSISSSSLVQKDKSITAVVESVRLP---GASHIVKGVITTNLLALKQKQNGRS		446	LOPRYYSISSSSLVQKDKSITAVVESVRLP---GASHIVKGVITTNLLALKQKQNGRS
	yeast	436	LOPRYYSISSSSLVQKDKSITAVVESVRLP-DAPPGVGVTNTLLRNICLAQNNVNI		436	LOPRYYSISSSSLVQKDKSITAVVESVRLP-DAPPGVGVTNTLLRNICLAQNNVNI

5	PMON45605	503	-----NGGR-----ALVPMFVRKSQFRLPFKA TPVIMVGP GTGVAPF IGFIQE
	human	503	-----NGGR-----ALVPMFVRKSQFRLPFKA TPVIMVGP GTGVAPF IGFIQE
	mouse	503	-----NGGR-----ALVPMFVRKSQFRLPFKA TPVIMVGP GTGVAPF IGFIQE
	pMON45632	505	PDPHG TYSITGPRNKYDGITHVHVVR SNFILPSDPSRPV IMVGP GTGVAPF MGFIQE
	niger	503	SRPSR-LD LHHGPRNKYDGITHVHVVR SNFILPSDPSRPV IMVGP GTGVAPF RGFIQE
	yeast	495	AETNLPVHYDLINGPRKL ANYK P HVRRSNFRLPSNP STPVIM GP GTGVAPF RGFIQE
10	PMON45605	547	RAWLRQ---OGKE---VGETLL YGCRRSDED LYREELAOFHED-GALTQLNVAFSRE-
	human	547	RAWLRQ---OGKE---VGETLL YGCRRSDED LYREELAOFHED-GALTQLNVAFSRE-
	mouse	547	RAWLRQ---OGKE---VGETLL YGCRRSDED LYREELAOFHED-GALTQLNVAFSRE-
	pMON45632	564	RAALAA---KGEK---VGTTLL YGCRRSDED LYREELAOFHED-GALTQLNVAFSRE-
	niger	562	RAALAA---KGEK---VGPTVLEEGCRKSDED LYREELAOFHED-GALTQLNVAFSRE-
	yeast	555	RVAFLESQKKCGNNVSLGKH LEYGSRN D DLYQDEWPE ANKLDSFEMVVAHSRLP
15	PMON45605	599	OSHKVYYQHLLK DREH WKLT EGGAHIYVCGDARNMARDVQNTFYDIVAELG CAMEHAQ
	human	599	OSHKVYYQHLLK DREH WKLT EGGAHIYVCGDARNMARDVQNTFYDIVAELG CAMEHAQ
	mouse	599	OSHKVYYQHLLK DREH WKLT EGGAHIYVCGDARNMARDVQNTFYDIVAELG CAMEHAQ
	pMON45632	617	SAEKVYYQFRLR EHLVSDL KQKATFYVCGDAANMARDVQNTFYDIVAELG CAMEHAQ
	niger	615	GPKVYYQFRLR EHLVSDL KQKATFYVCGDAANMARDVQNTFYDIVAELG CAMEHAQ
	yeast	614	NPKVYYQDKL KDYEDQVFEM NNGAFIYVCGDAKGMAGV STALVG LSRGKS TTD
25	PMON45605	658	AVDY KKLMTKGRY SLDVWS
	human	658	AVDY KKLMTKGRY SLDVWS
	mouse	659	AVDY KKLMTKGRY SLDVWS
	pMON45632	676	DEPMVK MRSGSYQDDVWS
	niger	674	DEPMVK MRSGRYQEDVWS
30	yeast	673	ATEL KMLKT SGRYQEDVWS
35	PMON45605	(SEQ ID NO: 03)	
	human	(SEQ ID NO: 06)	
	mouse	(SEQ ID NO: 39)	
	PMON45632	(SEQ ID NO: 05)	
	niger	(SEQ ID NO: 38)	
	yeast	(SEQ ID NO: 37)	

Figure 8 – Amino acid homology alignment of *A. ochraceus* oxidoreductase to NADPH cytochrome P450 reductases from *A. niger* and *S. cerevisiae*

5	A. niger	1	-MAOLDTLVLLVLA V LLVGSVAYFTKGT Y WAVAK E RMP L PAPR M N C A K AK K T R D I E KKM
	A. ochraceus	1	-MAOLDTLVLLVLA V LLVGSVAYFTKGT Y WAVAK D PY S A G P A M N C A K A G K T R D I E QKM
	S. cerevisiae	1	MPFG D N T D F T V LAGL V AV V LYVK I N S KE L LM S DD G DITAVSSG ----- NRDIAQV
10	A. niger	60	E TGKNCVIFYGSQTGT A EDYASRLAKEGSQR F GLK T M V AD L E D Y V E N L E OF P E D K V A F
	A. ochraceus	60	DETGKNCVIFYGSQTGT A EDYASRLAKEGSQR F GLK T M V AD L E D Y V E N L E KE F P E D K V F
	S. cerevisiae	55	TEN N K N V LY V Y S QTGT A EDY A K F S K E L V A K F N L N V MA D Y V E N D E S I ND V P ----- V V V S
15	A. niger	120	FV L ATY G E G P T D N A V E F Y Q F T G D D V A F E S A - AS A D E K P L S K L K Y V A F G L G N N T Y E H Y N A -
	A. ochraceus	120	FV L ATY G E G P T D N A V E F Y Q F T G D D V A F E S A - AD D K L S L K Y V A F G L G N N T Y E H Y N A -
	S. cerevisiae	113	IF E T Y G E F P D G A V N E E F I C - NA A G A L S N L T N M T G L G N S T Y E F I E N G
20	A. niger	179	MVR Q V D A A F O K L G P Q R I G S A G E G D G A G T M E E D F L W K P E M W A A L S E S M D L E E A V Y E P
	A. ochraceus	180	MVR Q V D A A F O K L G P Q R I G S A G E G D G A G T M E E D F L W K P E M W A A L S E S M D L E E A V Y E P
	S. cerevisiae	163	AA A K A K H I S A A G A I R K G L G E + DD G A T T E D E X A W K S I L E V L K E B E H L D E Q E A K T S
25	A. niger	239	VFC V T E N E S L S P E D E T V V L G E P T O SH Q - -----G I P K G P Y S A H N P F I A P I A E S R E L -
	A. ochraceus	240	V F N V T E N E S L S P E D E T V V L G E P T O SH Q - -----G I P K G P Y S A H N P F I A P I A E S R E L -
	S. cerevisiae	223	Q F O Y T - VL N E I T D S S L G E P S A H Y L I PS Q SH Q LN R NA D G I QL G P E D L S O P I A P I V R S R E L -
30	A. niger	290	F T V K DR N CL H ME I S I AG S N L T Y Q T G D H I A W V P T N A G E V D R F L Q V G L E G K R E S V NI K G -
	A. ochraceus	291	F T V K DR N CL H ME I S I AG S N L T Y Q T G D H I A W V P T N A G E V D R F L Q V G L E G K R E S V NI K G -
	S. cerevisiae	280	F S S N D R N C H SE F D E S G S N I K Y S T G D H I A W V P E N P L E K V E Q F L S I P N L D P - E I F D E K P -
35	A. niger	350	ID V T A K V P I P T P T Y D A A V R Y Y E V C A P V S R Q F V T AT L A A F P M R K A R O R L C W E Q G - LF -
	A. ochraceus	351	ID V T A K V P I P T P T Y D A A V R Y Y E V C A P V S R Q F V T ST L A A F P D E A T A E V V R L G C D D Y F
	S. cerevisiae	338	ID P T V K V F P T P T I C A A M Y H L E T G P V S R Q L F S SS I Q F P N AD V E K R L T E L S K D K Q F -
40	A. niger	409	P R E G H P M L Q H A Q A L Q S I T - K P F A V P F S L L I E G I T K L Q P R Y Y S I S S S L V Q K D K I S I T -
	A. ochraceus	411	HE K I T H C F N I A Q A L Q S I T - K P F A V P F S L L I E G I T K L Q P R Y Y S I S S S L V Q K D K I S I T -
	S. cerevisiae	398	A V E I T S K Y F N I A D A K Y - SD G A K DN V M Q F L S E S P Q Y T P R Y S I S S S L S E K O T H V I T -
45	A. niger	468	AV V E S V R L P --G A S H E V K G V T T N Y N L L A L K Q K Q N G R S SR P SR R SR - I D L L H H G P R N K Y D G I H V -
	A. ochraceus	470	AV V E S V R L P --G A S H E V K G V T T N Y N L L A L K Q K Q N G R S SR P SR R SR - I D L L H H G P R N K Y D G I H V -
	S. cerevisiae	458	STE V N F P N E L P A P P G V G V T T LR N Q L A Q N N V N TA T N L P M H I D N G P R K L A N Y K -
50	A. niger	525	PV H V R H S N F K L P S D P SR P IM V G P G T GV A P F R G F I Q E R A A A L A A A K G E K - V C E P T V L F
	A. ochraceus	527	PV H V R H S N F K L P S D P SR P V I M V G P G T GV A P F R G F I Q E R A A A L A A A K G E K - V C E P T V L F
	S. cerevisiae	518	PV H V R H S N F K L P S D P SR P V I M V G P G T GV A P F R G F I Q E R A A A L A A A K G E K - V C E P T V L F
	A. niger	579	FG C R K S D E D F L Y K D E W K T Y Q O Q L G D N L K I I T A F S R E - G P Q K V V V Q H R L R E H S E L V S D L L K -
	A. ochraceus	581	FG C R K S D E D F L Y K D E W K T Y Q O Q L G D N L K I I T A F S R E - S A E K V V V Q H R L R E H A E L V S D L L K -
	S. cerevisiae	578	Y G S R N E D - DF L Y D E W P E Y A K L D G S F E N V A H S R L P N T K V V Q D Y K D Y E D Q V E M N
	A. ochraceus, PMON45632	(SEQ ID NO: 05)	
	A. niger	(SEQ ID NO: 38)	
	S. cerevisiae, yeast	(SEQ ID NO: 37)	

**Figure 9 – Phylogenetic tree showing the relatedness of
Aspergillus ochraceus and human oxidoreductase to
reductases from A. niger, yeast, and mouse.**

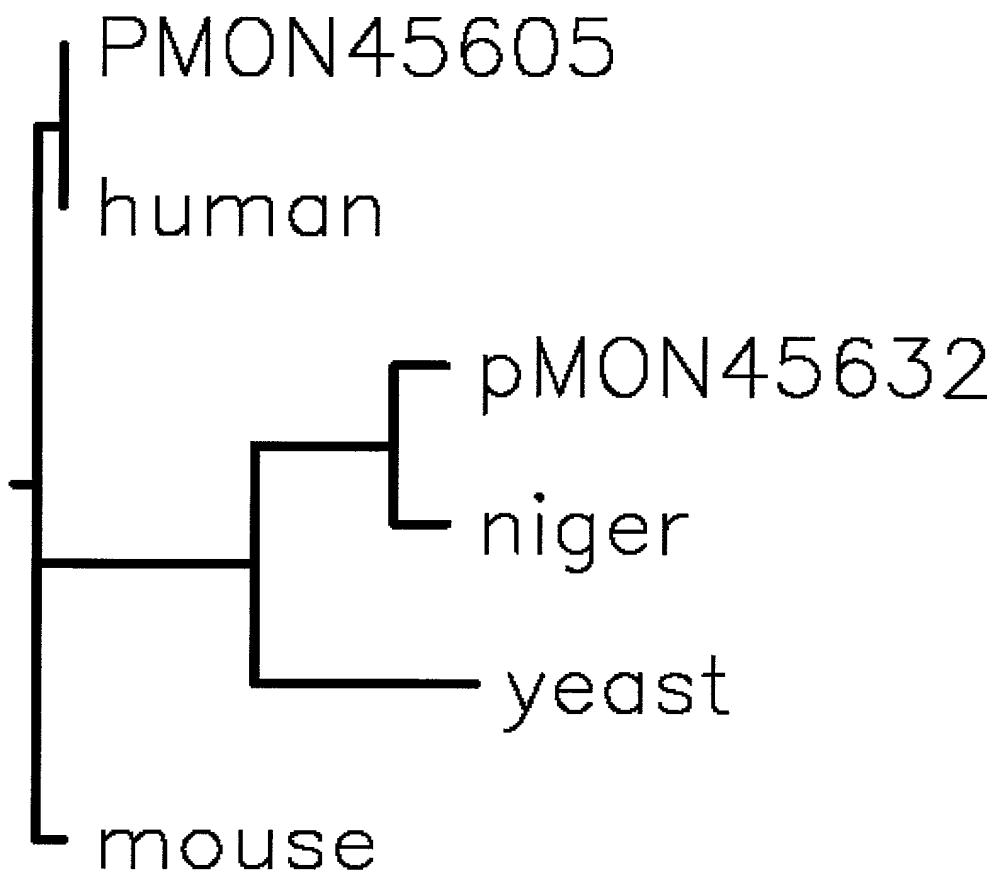


Figure 10 – Percent homology between *Aspergillus ochraceus* oxidoreductase to reductases from *A. niger*, yeast, and mouse and human.

Accession number	organism	% id to A.och oxred
CAA81550	<i>A. niger</i>	84
BAA02936	<i>S. cerevisiae</i>	37
BAA04496	mouse	34
AAB21814	human	33

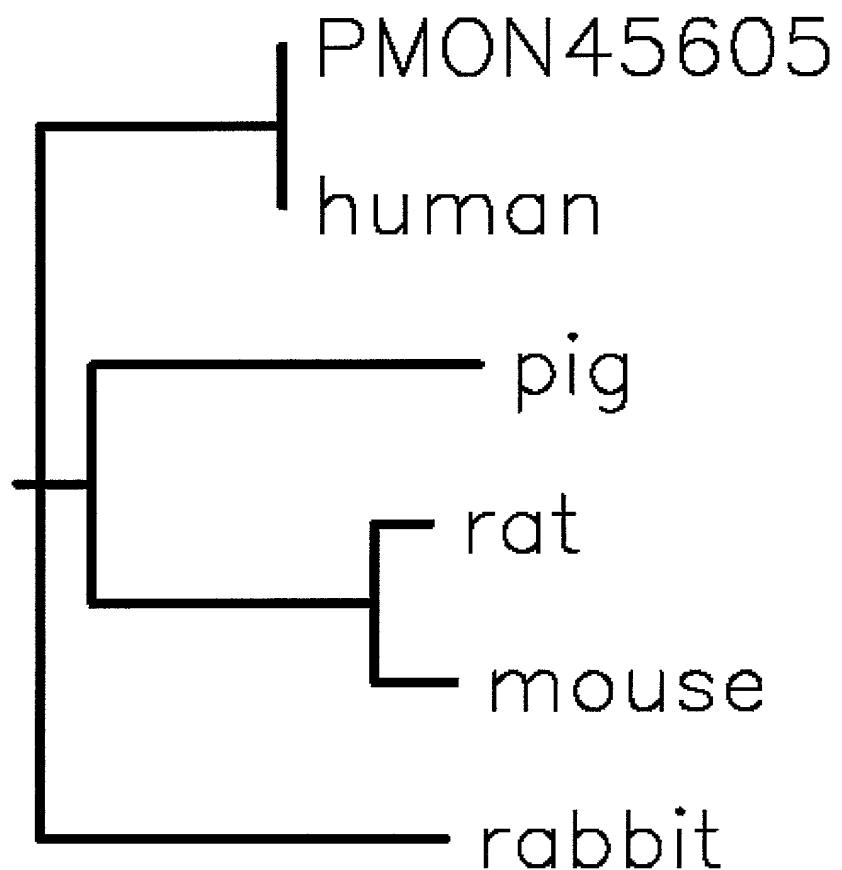
Figure 11 – Amino acid homology alignment of human oxidoreductase with the top 4 hits from SwissProt

	PMON45605	1	MGDSHVDTSEAVAEVSLFSMTDM LFSLIVGLLTYWFEFRKKKEEVPEF SKIQTL
5	human	1	MGDSHVDTSEAVAEVSLFSMTDM LFSLIVGLLTYWFEFRKKKEEVPEF SKIQTL
	rabbit	1	MADSHEDIGATPEAAQAEASVFSMTD VLFSLIVGLLTYWFEFRKKKEEVPEF SKIQAP
	rat	1	MGDSHEDTSATMP PEAAFEVSLFS TDMVLFSLIVGLLTYWFEFRKKKEEVPEF SKIQTT
	mouse	1	MGDSHEDTSATVPEAAEVSLF STTDVLFSLIVGLLTYWFEFRKKKEEVPEF SKIQTT
10	pig	1	MGDSNVDTGTTSE MVAEEVSLFS ATDMVLFSLIVGLLTYWFEFRKKKEEVPEF SKIETT
	PMON45605	61	TSS VRESSFVEKMKTGRNIIVFYGSQTGTAEFFANRLSKDAHRYGMRGMSADPEEYDL
	human	61	TSS VRESSFVEKMKTGRNIIVFYGSQTGTAEFFANRLSKDAHRYGMRGMSADPEEYDL
	rabbit	61	TSSVKESSFVEKMKTGRNIIVFYGSQTGTAEFFANRLSKDAHRYGMRGMSADPEEYDL
15	rat	61	APP VKESSFVEKMKTGRNIIVFYGSQTGTAEFFANRLSKDAHRYGMRGMSADPEEYDL
	mouse	61	APP VKESSFVEKMKTGRNIIVFYGSQTGTAEFFANRLSKDAHRYGMRGMSADPEEYDL
	pig	61	TSSVKESSFVEKMKTGRNIIVFYGSQTGTAEFFANRLSKDAHRYGMRGMSADPEEYDL
20	PMON45605	120	ADLSSLPEIDNALVVFCMATYGEVDPTDNAQDFYDWLQETDVDSLGVKFAVFG GLGNKTYE
	human	120	ADLSSLPEIDNALVVFCMATYGEVDPTDNAQDFYDWLQETDVDSLGVKFAVFG GLGNKTYE
	rabbit	121	ADLSSLPEIDNALAVFCMATYGEVDPTDNAQDFYDWLQETDVDSLGVKFAVFG GLGNKTYE
	rat	120	ADLSSLPEIDKSLVVFCMATYGEVDPTDNAQDFYDWLQETDVDSLGVKFAVFG GLGNKTYE
	mouse	120	ADLSSLPEIDKSLVVFCMATYGEVDPTDNAQDFYDWLQETDVDSLGVKFAVFG GLGNKTYE
25	pig	120	SDLSSLPEIDNALAVFCMATYGEVDPTDNAQDFYDWLQEA DVDSLGVKFAVFG GLGNKTYE
	PMON45605	180	HFNAMGKYVDK RLEQLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFG VEATGEE
	human	180	HFNAMGKYVDK RLEQLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFG VEATGEE
30	rabbit	181	HFNAMGKYVDQ RLEQLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFG VEATGEE
	rat	180	HFNAMGKYVDQ RLEQLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEFFG VEATGEE
	mouse	180	HFNAMGKYVDQ RLEQLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEFFG VEATGEE
	pig	180	HFNAMGKYVDK RLEQLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFG VEATGEE
35	PMON45605	240	SSIROYELVVHTD DAAKVYMGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
	human	240	SSIROYELVVHTD DAAKVYMGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
	rabbit	241	SSIROYELV HTD DAAKVYQGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
	rat	240	SSIROYELVVHEDMD DAAKVYTGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
40	mouse	240	SSIROYELVVHEDMD DAAKVYTGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
	pig	240	SSIROYELVVHTD DAAKVYTGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
	PMON45605	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGK ILGADLDVVM MSLNNLDEESNKKH
45	human	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGK ILGADLDVVM MSLNNLDEESNKKH
	rabbit	301	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGK GEILGADLDV MSLNNLDEESNKKH
	rat	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGK GEILGADLDV MSLNNLDEESNKKH
	mouse	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGK GEILGADLDV MSLNNLDEESNKKH
50	pig	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGK GEILGADLDV MSLNNLDEESNKKH
	PMON45605	360	PFPCTSYRTALTYYL DITNPRTNVLYELAQYASEPSEQEL LRKMASSSGEGKELYLSW
	human	360	PFPCTSYRTALTYYL DITNPRTNVLYELAQYASEPSEQEL LRKMASSSGEGKELYLSW
	rabbit	361	PFPCTSYRTALTYYL DITNPRTNVLYELAQYADP AEQELRKMASSSGEGKELYLSW
55	rat	360	PFPCTSYRTALTYYL DITNPRTNVLYELAQYASEPSEOEHL LRKMASSSGEGKELYLSW

mouse	360	PFP CPT YRT ALTY YLD ITN P PRT NVL YEL A QY A S E P S E Q E H KMA S S GEG K E L Y L S W
pig	360	PFP CPT YRT ALTY YLD ITN P PRT NVL YEL A QY A S E P S E Q E Q L R KMA S S GEG K E L Y L S W
5	PMON45605	420 VVEARRHILAILQDCPSLRPPIDHLCELLPRLQARYYSTASSSKVHPNSVHICAVVVEYE
	human	420 VVEARRHILAILQDCPSLRPPIDHLCELLPRLQARYYSTASSSKVHPNSVHICAVVVEYE
	rabbit	421 VVEARRHILAILQDYP SLRPPIDHLCELLPRLQARYYSTASSSKVHPNSVHICAVVVEYE
	rat	420 VVEARRHILAILQDYP SLRPPIDHLCELLPRLQARYYSTASSSKVHPNSVHICAVVVEYE
10	mouse	420 VVEARRHILAILQDYP SLRPPIDHLCELLPRLQARYYSTASSSKVHPNSVHICAVVVEYE
	pig	420 VVEARRHILAILQDYP SLRPPIDHLCELLPRLQARYYSTASSSKVHPNSVHICAVVVEYE
15	PMON45605	480 TKA GR I N K G V A T N W L R A K E P A G E N G G R A L V P M F V R K S Q F R L P F K A T T P V I M V G P G T G V A P
	human	480 TKA GR I N K G V A T N W L R A K E P A G E N G G R A L V P M F V R K S Q F R L P F K A T T P V I M V G P G T G V A P
	rabbit	481 TKA GR I N K G V A T S W L R A K E P A G E N G G R A L V P M F V R K S Q F R L P F K A T T P V I M V G P G T G V A P
	rat	480 A K S G R V N K G V A T S W L R A K E P A G E N G G R A L V P M F V R K S Q F R L P F K P T T P V I M V G P G T G I A P
	mouse	480 A K S G R V N K G V A T S W L R T K E P A G E N G R A L V P M F V R K S Q F R L P F K P T T P V I M V G P G T G V A P
	pig	480 T K S G R V N K G V A T S W L R A K E P A G E N G R A L V P M F V R K S Q F R L P F K A T T P V I M V G P G T G V A P

5	PMON45605	540	FIGFIGERAWLREQGKEVGETLLYYGCRSSDEDYLYREELAQFHRDGALTQLNVAFSREQ
	human	540	FIGFIGERAWLREQGKEVGETLLYYGCRSSDEDYLYREELAQFHRDGALTQLNVAFSREQ
	rabbit	541	FIGFIGERAWLREQGKEVGETLLYYGCRSSDEDYLYREELAQFHRDGALTQLNVAFSREQ
	rat	540	FIGFIGERAWLREQGKEVGETLLYYGCRSSDEDYLYREELAQFHKDGALTQLNVAFSREQ
	mouse	540	FIGFIGERAWLREQGKEVGETLLYYGCRSSDEDYLYREELAQFHKDGALTQLNVAFSREQ
	pig	540	FIGFIGERAWLREQGKEVGETLLYYGCRSSDEDYLYREELAQFHKGALTRLSVAFSREQ
10	PMON45605	600	SHKVVVQHLLKDRREHLWKLIDEGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQA
	human	600	SHKVVVQHLLKDRREHLWKLIDEGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQA
	rabbit	601	AOKVVVQHLLKDRREHLWKLIDHEGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQA
	rat	600	AHKVVVQHLLKDRREHLWKLIDHEGGAHIYVCGDARNMARDVQNTFYDIVAEGPMEHTQA
	mouse	600	AHKVVVQHLLKDRREHLWKLIDHEGGAHIYVCGDARNMARDVQNTFYDIVAEGPMEHTQA
	pig	600	POKVVVQHLLKDRREHLWKLIDEGGAHIYVCGDARNMARDVQNTFCDIVAEQGPMEHAQA
15	PMON45605	659	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 03)
	human	659	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 52)
	rabbit	661	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 53)
20	rat	660	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 54)
	mouse	660	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 55)
	pig	660	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 56)

Figure 12 – Phylogenetic tree showing the relatedness of human oxidoreductase (P16435) with top 4 hits from SwissProt



**Figure 13 – Percent homology between human oxidoreductase
and top 4 hits from SwissProt**

Accession number	Species	% id to human oxred
P00388	rat	92
P00389	rabbit	92
P37040	mouse	92
P04175	pig	91

Figure 14 - Expression of Aspergillus ochraceus 11 alpha hydroxylase in transfected Sf9 insect cells

Expression of 11- α -Hydroxylase in Transfected Sf9 Cells

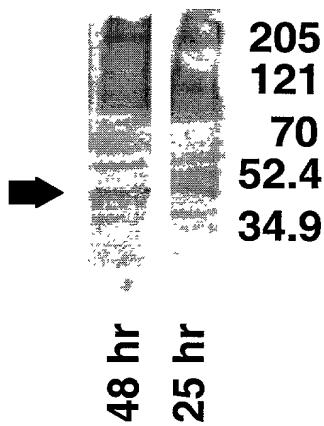


Figure 15 - Expression of Aspergillus ochraceus P450 oxidoreductase in transfected Sf9 insect cells

Expression of Fungal P-450 Oxidoreductase in Transfected Sf9 Cells

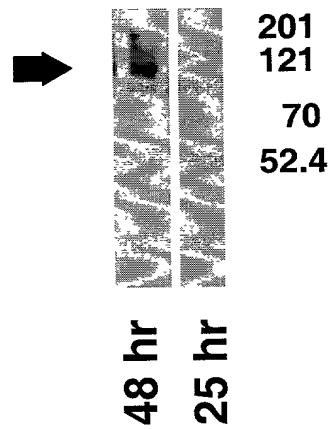


Figure 16 - Conversion of androstenedione to 11 alpha hydroxy androstenedione monitored by HPLC

